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RAW SEQUENCE LISTING

DATE: 04/11/2002

PATENT APPLICATION: US/10/020,139

TIME: 09:17:39

Input Set : N:\Crf3\RULE60\10020139.raw

Output Set: N:\CRF3\04112002\J020139.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:
5 (i) APPLICANT: DUAN, ROXANNE
6 RUBEN, STEVEN
8 (ii) TITLE OF INVENTION: Parotid Secretory Protein
10 (iii) NUMBER OF SEQUENCES: 18
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: HUMAN GENOME SCIENCES, INC.
14 (B) STREET: 9410 KEY WEST AVENUE
15 (C) CITY: ROCKVILLE
16 (D) STATE: MD
17 (E) COUNTRY: US
18 (F) ZIP: 20850
20 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: Floppy disk
22 (B) COMPUTER: IBM PC compatible
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
26 (vi) CURRENT APPLICATION DATA:
C--> 27 (A) APPLICATION NUMBER: US/10/020,139
C--> 28 (B) FILING DATE: 18-Dec-2001
29 (C) CLASSIFICATION:
31 (vii) PRIOR APPLICATION DATA:
32 (A) APPLICATION NUMBER: US/08/993,529
33 (B) FILING DATE:
36 (viii) ATTORNEY/AGENT INFORMATION:
37 (A) NAME: BROOKES, ANDERS A.
38 (B) REGISTRATION NUMBER: 36,373
39 (C) REFERENCE/DOCKET NUMBER: PF348
41 (ix) TELECOMMUNICATION INFORMATION:
42 (A) TELEPHONE: (301) 309-8504
43 (B) TELEFAX: (301) 301-8439
46 (2) INFORMATION FOR SEQ ID NO: 1:
48 (i) SEQUENCE CHARACTERISTICS:
49 (A) LENGTH: 1028 base pairs
50 (B) TYPE: nucleic acid
51 (C) STRANDEDNESS: single
52 (D) TOPOLOGY: linear
54 (ii) MOLECULE TYPE: DNA (genomic)
57 (ix) FEATURE:
58 (A) NAME/KEY: CDS
59 (B) LOCATION: 49..795
61 (ix) FEATURE:

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Output Set: N:\CRF3\04112002\J020139.raw

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62      (A) NAME/KEY: sig_peptide
63      (B) LOCATION: 49..100
65      (ix) FEATURE:
66      (A) NAME/KEY: mat_peptide
67      (B) LOCATION: 103..795
70      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
72 CACGAGATTT CATGAGCATC CTCCTCTAAA CGCGTGTCAG GACAAAAG ATG CTT CAG      57
73                                     Met Leu Gln
74                                     -18
76 CTT TGG AAA CTT GTT CTC CTG TGC GGC GTG CTC ACT GGG ACC TCA GAG      105
77 Leu Trp Lys Leu Val Leu Leu Cys Gly Val Leu Thr Gly Thr Ser Glu
W--> 78 -15      -10      -5      1
80 TCT CTT CTT GAC AAT CTT GGC AAT GAC CTA AGC AAT GTC GTG GAT AAG      153
81 Ser Leu Leu Asp Asn Leu Gly Asn Asp Leu Ser Asn Val Val Asp Lys
82      5      10      15
84 CTG GAA CCT GTT CTT CAC GAG GGA CTT GAG ACA GTT GAC AAT ACT CTT      201
85 Leu Glu Pro Val Leu His Glu Gly Leu Glu Thr Val Asp Asn Thr Leu
86      20      25      30
88 AAA GGC ATC CTT GAG AAA CTG AAG GTC GAC CTA GGA GTG CTT CAG AAA      249
89 Lys Gly Ile Leu Glu Lys Leu Lys Val Asp Leu Gly Val Leu Gln Lys
90      35      40      45
92 TCC AGT GCT TGG CAA CTG GCC AAG CAG AAG GCC CAG GAA GCT GAG AAA      297
93 Ser Ser Ala Trp Gln Leu Ala Lys Gln Lys Ala Gln Glu Ala Glu Lys
94 50      55      60      65
96 TTG CTG AAC AAT GTC ATT TCT AAG CTG CTT CCA ACT AAC ACG GAC ATT      345
97 Leu Leu Asn Asn Val Ile Ser Lys Leu Leu Pro Thr Asn Thr Asp Ile
98      70      75      80
100 TTT GGG TTG AAA ATC AGC AAC TCC CTC ATC CTG GAT GTC AAA GCT GAA      393
101 Phe Gly Leu Lys Ile Ser Asn Ser Leu Ile Leu Asp Val Lys Ala Glu
102      85      90      95
104 CCG ATC GAT GAT GGC AAA GGC CTT AAC CTG AGC TTC CCT GTC ACC GCG      441
105 Pro Ile Asp Asp Gly Lys Gly Leu Asn Leu Ser Phe Pro Val Thr Ala
106      100      105      110
108 AAT GTC ACT GTG GCC GGG CCC ATC ATT GGC CAG ATT ATC AAC CTG AAA      489
109 Asn Val Thr Val Ala Gly Pro Ile Ile Gly Gln Ile Ile Asn Leu Lys
110      115      120      125
112 GCC TCC TTG GAC CTC CTG ACC GCA GTC ACA ATT GAA ACT GAT CCC CAG      537
113 Ala Ser Leu Asp Leu Leu Thr Ala Val Thr Ile Glu Thr Asp Pro Gln
114 130      135      140      145
116 ACA CAC CAG CCT GTT GCC GTC CTG GGA GAA TGC GCC AGT GAC CCA ACC      585
117 Thr His Gln Pro Val Ala Val Leu Gly Glu Cys Ala Ser Asp Pro Thr
118      150      155      160
120 AGC ATC TCA CTT TCC TTG CTG GAC AAA CAC AGC CAA ATC ATC AAC AAG      633
121 Ser Ile Ser Leu Ser Leu Leu Asp Lys His Ser Gln Ile Ile Asn Lys
122      165      170      175
124 TTC GTG AAT AGC GTG ATC AAC ACG CTG AAA AGC ACT GTA TCC TCC CTG      681
125 Phe Val Asn Ser Val Ile Asn Thr Leu Lys Ser Thr Val Ser Ser Leu
126      180      185      190
128 CTG CAG AAG GAG ATA TGT CCA CTG ATC CGC ATC TTC ATC CAC TCC CTG      729

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129 Leu Gln Lys Glu Ile Cys Pro Leu Ile Arg Ile Phe Ile His Ser Leu
130      195                200                205
132 GAT GTG AAT GTC ATT CAG CAG GTC GTC GAT AAT CCT CAG CAC AAA ACC      777
133 Asp Val Asn Val Ile Gln Gln Val Val Asp Asn Pro Gln His Lys Thr
134 210                215                220                225
136 CAG CTG CAA ACC CTC ATT TGAAGAGGAC GAATGAGGAG GACCACTGTG      825
137 Gln Leu Gln Thr Leu Ile
138      230
140 GTGCATGCTG ATTGGTTCCC AGTGGCTTGC CCCACCCCCT TATAGCATCT CCCTCCAGGA      885
142 AGCTGCTGCC ACCACCTAAC CAGCGTGAAA GCCTGAGTCC CACCAGAAGG ACCTTCCAG      945
144 ATACCCCTTC TCCTCACAGT CAGAACAGCA GCCTCTACAC ATGTTGTCCT GCCCTGGCA      1005
146 ATAAAGGCC ATTTCTGCAA AAA      1028
149 (2) INFORMATION FOR SEQ ID NO: 2:
151      (i) SEQUENCE CHARACTERISTICS:
152          (A) LENGTH: 249 amino acids
153          (B) TYPE: amino acid
154          (D) TOPOLOGY: linear
156      (ii) MOLECULE TYPE: protein
158      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
160 Met Leu Gln Leu Trp Lys Leu Val Leu Leu Cys Gly Val Leu Thr Gly
161 -18      -15      -10      -5
163 Thr Ser Glu Ser Leu Leu Asp Asn Leu Gly Asn Asp Leu Ser Asn Val
164      1      5      10
166 Val Asp Lys Leu Glu Pro Val Leu His Glu Gly Leu Glu Thr Val Asp
167 15      20      25      30
169 Asn Thr Leu Lys Gly Ile Leu Glu Lys Leu Lys Val Asp Leu Gly Val
170      35      40      45
172 Leu Gln Lys Ser Ser Ala Trp Gln Leu Ala Lys Gln Lys Ala Gln Glu
173      50      55      60
175 Ala Glu Lys Leu Leu Asn Asn Val Ile Ser Lys Leu Leu Pro Thr Asn
176      65      70      75
178 Thr Asp Ile Phe Gly Leu Lys Ile Ser Asn Ser Leu Ile Leu Asp Val
179      80      85      90
181 Lys Ala Glu Pro Ile Asp Asp Gly Lys Gly Leu Asn Leu Ser Phe Pro
182 95      100      105      110
184 Val Thr Ala Asn Val Thr Val Ala Gly Pro Ile Ile Gly Gln Ile Ile
185      115      120      125
187 Asn Leu Lys Ala Ser Leu Asp Leu Leu Thr Ala Val Thr Ile Glu Thr
188      130      135      140
190 Asp Pro Gln Thr His Gln Pro Val Ala Val Leu Gly Glu Cys Ala Ser
191      145      150      155
193 Asp Pro Thr Ser Ile Ser Leu Ser Leu Leu Asp Lys His Ser Gln Ile
194      160      165      170
196 Ile Asn Lys Phe Val Asn Ser Val Ile Asn Thr Leu Lys Ser Thr Val
197 175      180      185      190
199 Ser Ser Leu Leu Gln Lys Glu Ile Cys Pro Leu Ile Arg Ile Phe Ile
200      195      200      205
202 His Ser Leu Asp Val Asn Val Ile Gln Gln Val Val Asp Asn Pro Gln
203      210      215      220

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205 His Lys Thr Gln Leu Gln Thr Leu Ile
206      225      230
208 (2) INFORMATION FOR SEQ ID NO: 3:
210   (i) SEQUENCE CHARACTERISTICS:
211       (A) LENGTH: 235 amino acids
212       (B) TYPE: amino acid
213       (C) STRANDEDNESS: single
214       (D) TOPOLOGY: linear
216   (ii) MOLECULE TYPE: protein
221   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
223   Met Phe Gln Leu Gly Ser Leu Val Val Leu Cys Gly Leu Leu Ile Gly
224     1             5             10             15
226   Asn Ser Glu Ser Leu Leu Gly Glu Leu Gly Ser Ala Val Asn Asn Leu
227             20             25             30
229   Lys Ile Leu Asn Pro Pro Ser Glu Ala Val Pro Gln Asn Leu Asn Leu
230             35             40             45
232   Asp Val Glu Leu Leu Gln Gln Ala Thr Ser Trp Pro Leu Ala Lys Asn
233             50             55             60
235   Ser Ile Leu Glu Thr Leu Asn Thr Ala Asp Leu Gly Asn Leu Lys Ser
236             65             70             75             80
238   Phe Thr Ser Leu Asn Gly Leu Leu Leu Lys Ile Asn Asn Leu Lys Val
239             85             90             95
241   Leu Asp Phe Gln Ala Lys Leu Ser Ser Asn Gly Asn Gly Ile Asp Leu
242             100            105            110
244   Thr Val Pro Leu Ala Gly Glu Ala Ser Leu Val Leu Pro Phe Ile Gly
245             115            120            125
247   Lys Thr Val Asp Ile Ser Val Ser Leu Asp Leu Ile Asn Ser Leu Ser
248             130            135            140
250   Ile Lys Thr Asn Ala Gln Thr Gly Leu Pro Glu Val Thr Ile Gly Lys
251             145            150            155            160
253   Cys Ser Ser Asn Thr Asp Lys Ile Ser Ile Ser Leu Leu Gly Arg Arg
254             165            170            175
256   Leu Pro Ile Ile Asn Ser Ile Leu Asp Gly Val Ser Thr Leu Leu Thr
257             180            185            190
259   Ser Thr Leu Ser Thr Val Leu Gln Asn Phe Leu Cys Pro Leu Leu Gln
260             195            200            205
262   Tyr Val Leu Ser Thr Leu Asn Pro Ser Val Leu Gln Gly Leu Leu Ser
263             210            215            220
265   Asn Leu Leu Ala Gly Gln Val Gln Leu Ala Leu
266             225            230            235
268 (2) INFORMATION FOR SEQ ID NO: 4:
270   (i) SEQUENCE CHARACTERISTICS:
271       (A) LENGTH: 235 amino acids
272       (B) TYPE: amino acid
273       (C) STRANDEDNESS: single
274       (D) TOPOLOGY: linear
276   (ii) MOLECULE TYPE: protein
281   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
283   Met Phe Gln Leu Gly Ser Leu Val Val Leu Cys Gly Leu Leu Ile Gly

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284      1              5              10              15
286  Thr Ser Glu Ser Leu Leu Gly Asp Val Ala Asn Ala Val Asn Asn Leu
287              20              25              30
289  Asp Ile Leu Asn Ser Pro Ser Glu Ala Val Ala Gln Asn Leu Asn Leu
290              35              40              45
292  Asp Val Gly Ser Leu Gln Gln Ala Thr Thr Trp Pro Ser Ala Lys Asp
293              50              55              60
295  Ser Ile Leu Glu Thr Leu Asn Lys Val Glu Leu Gly Asn Ser Asn Gly
296              65              70              75              80
298  Phe Thr Pro Leu Asn Gly Leu Leu Leu Arg Val Asn Lys Phe Arg Val
299              85              90              95
301  Leu Asp Leu Gln Ala Gly Leu Ser Ser Asn Gly Lys Asp Ile Asp Leu
302              100              105              110
304  Lys Leu Pro Leu Val Phe Glu Ile Ser Phe Ser Leu Pro Val Ile Gly
305              115              120              125
307  Pro Thr Leu Asp Val Ala Val Ser Leu Asp Leu Leu Asn Ser Val Ser
308              130              135              140
310  Val Gln Thr Asn Ala Gln Thr Gly Leu Pro Gly Val Thr Leu Gly Lys
311              145              150              155              160
313  Cys Ser Gly Asn Thr Asp Lys Ile Ser Ile Ser Leu Leu Gly Arg Arg
314              165              170              175
316  Leu Pro Phe Val Asn Arg Ile Leu Asp Gly Val Ser Gly Leu Leu Thr
317              180              185              190
319  Gly Ala Val Ser Ile Leu Leu Gln Asn Ile Leu Cys Pro Val Leu Gln
320              195              200              205
322  Tyr Leu Leu Ser Thr Met Ser Gly Ser Ala Ile Gln Gly Leu Leu Ser
323              210              215              220
325  Asn Val Leu Thr Gly Gln Leu Ala Val Pro Leu
326              225              230              235

```

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 206 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```

343  Met Phe Gln Leu Gly Ser Leu Val Val Leu Cys Gly Leu Leu Ile Gly
344      1              5              10              15
346  Thr Ser Gly Ser Leu Phe Asp Ile Phe Gln Asn Pro Glu Leu Asp Val
347              20              25              30
349  Glu Ser Val Trp Ser Glu Ile Asn Tyr Arg Ile Arg Tyr Ala Leu Glu
350              35              40              45
352  Thr Met Asp Leu Asp Met Leu Ala Asp Tyr Leu Ser Lys Arg Gly Ile
353              50              55              60
355  Glu Leu Lys Ile Lys Asp Leu Arg Ile Leu Asn Leu Asn His Glu Val
356              65              70              75              80
358  Ser Pro Asn Gly Asp Glu Val Thr Leu Lys Met Pro Met Ala Leu Asn
359              85              90              95

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/020,139

DATE: 04/11/2002

TIME: 09:17:40

Input Set : N:\Crf3\RULE60\10020139.raw

Output Set: N:\CRF3\04112002\J020139.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:78 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1